RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: ___10/004,115___

Source: ___OIPE___

Date Processed by STIC: ___8/12/0___

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PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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Revised 01/29/2002

OIPE

RAW SEQUENCE LISTING   DATE: 08/12/2002
PATENT APPLICATION: US/10/004,115   TIME: 16:10:55

Input Set : A:\72249.txt
Output Set: N:\CRF4\08122002\J004115.raw

```
    4 <110> APPLICANT: ASAKO, HIROYUKI
    5        MATSUMURA, KENJI
    6        SHIMIZU, MASATOSHI
    7        ITO, NOBUYA
    8        WAKITA, RYUHEI
   10 <120> TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
   11        4-HALO-3-HYDROXYBUTANOATE
   14 <130> FILE REFERENCE: 72249
   16 <140> CURRENT APPLICATION NUMBER: US 10/004,115
C--> 17 <141> CURRENT FILING DATE: 2002-08-05
   19 <150> PRIOR APPLICATION NUMBER: JP 2000-372704
   20 <151> PRIOR FILING DATE: 2000-12-07
   22 <150> PRIOR APPLICATION NUMBER: JP 2001-006144
   23 <151> PRIOR FILING DATE: 2001-01-15
   25 <150> PRIOR APPLICATION NUMBER: JP 2001-026594
   26 <151> PRIOR FILING DATE: 2001-02-02
   28 <150> PRIOR APPLICATION NUMBER: JP 2001-175175
   29 <151> PRIOR FILING DATE: 2001-06-11
   31 <160> NUMBER OF SEQ ID NOS: 33
   33 <170> SOFTWARE: FastSEQ for Windows Version 3.0
```

ERRORED SEQUENCES

```
  203 <210> SEQ ID NO: 6
  204 <211> LENGTH: 14
  205 <212> TYPE: PRT
  206 <213> ORGANISM: PENICILLIUM CITRINUM
  208 <400> SEQUENCE: 6
E--> 209  Tyr Glu Asp Val Leu Xaa Xaa Ile Asp Asp Ser Leu Lys Arg
  210    1                 5                  10
E--> 212 <210> SEQ ID NO: 8
  296 <210> SEQ ID NO: 15
  297 <211> LENGTH: 697
  298 <212> TYPE: DNA
  299 <213> ORGANISM: ESCHERICHIA COLI
  301 <400> SEQUENCE: 15
E--> 302  cgctctaaaa ctantggatc ccccgggctg caggaattcg gcggcggcgg atccaacgga      60
E--> 303  aanactttca cactgagcaa cggcgtcaaa attcctggcg tcggctttgg tacctncgct     120
E--> 304  agtgaaggtt ccaagggcga aacctatnct gctgtcacca ctgccctgaa aaccggttac     180
E--> 305  cgtcncttgg actgtgcctg gtactacctg aacaagggtg aggttggtga gggtntccgt     240
     306  gacttcctga aggaaaaccc ctcggtgaag cgtgaggaca tcttcgtctg caccaaggtg     300
E--> 307  tggaaccacc tccaccgtta tgaggacgtc ctctggtcca ttgacnactc cctgaagcgt     360
```

Xaa in sequence

Skipped sequence - step 3

See p. 4

n in sequence

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```
    308  cttggacttg actacgttga tatgttcctc gttcactggc ccattgctgc cgaaaaaaat    420
E--> 309  ggccagggtg agcccaaaat tggccctgac ggcaaatacn tcnttctcaa ggacctgacc    480
E--> 310  gaaancccna ncccacctgg cgcgctatgg aaaaaatttn tgangatccc aaggccaggt    540
E--> 311  ccattggtgt ttccaattgg accattgccg accttgagaa gatgtccaag ttngccaagg    600
E--> 312  tnatgcctca cgccaaccag atcgagattc accccttcct gcccaacgag gagctggtgc    660
E--> 313  agtactgctt ttccaagaac antatgcccg tagcgta                             697
    340  <210> SEQ ID NO: 18
    341  <211> LENGTH: 331
    342  <212> TYPE: DNA
    343  <213> ORGANISM: ESCHERICHIA COLI
    345  <400> SEQUENCE: 18
E--> 346  cgctctaaaa ctantggatc ccccgggctg caggaattcg gcggccgcgg atccttcatc     60
    347  cccatcatgt ctaacggaaa gactttcaca ttgagcaacg gcgtcaagat tcctggcgtc    120
    348  ggctttggta ccttcgctag tgaaggttcc aagggcgaga cctatactgc tgtcaccact    180
    349  gccctgaaga ccggttaccg tcacttggac tgtgcctggt actacctgaa cgagggtgag    240
    350  gttggtgagg gtatccgtga cttcctgaag gagaacccct cggtgaagcg tgaggacatc    300
    351  ttcgtctgca ccaaggtgtg gaaccacctc c                                   331
    353  <210> SEQ ID NO: 19
    354  <211> LENGTH: 743
    355  <212> TYPE: DNA
    356  <213> ORGANISM: ESCHERICHIA COLI
    358  <400> SEQUENCE: 19
    359  caaccagatc gagattcacc ccttcctgcc caacgaggag ctggtgcagt actgcttctc     60
    360  caagaacatt atgcccgtgg cctactctcc tctgggctcg cagaaccagg ttcccaccac    120
    361  cggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gcggcaacac    180
    362  ccttgctcag gttcttattg cctggggtct gcgccgtggc tacgtcgttc tccccaagag    240
    363  ctccaacccc aagcgcattg agtccaactt caagagcatt gagctctccg atgccgactt    300
    364  tgaagccatc aatgccgttg ccaagggtcg tcacttccgt ttcgtcaaca tgaaggatac    360
    365  tttcggatat gatgtctggc ccgaggagac cgccaagaac ctgtctgcgt gaatctctac    420
E--> 366  gaaattataa aatnacaccn acnaaaancc aaagcganag gatgatnccc aaaantttg     480
E--> 367  agggtttctt ggttgaaaac gtttantgan cccgaantga angaatagat gancntgatt    540
E--> 368  tctccaaaaa aaaaaaaaaa aaaaacggtc cgcggccgct ccnnggggg gcccggttcc     600
E--> 369  caattcnccc cttatnattg aattcttttt taangggnc aaattccncc nnatttccnt     660
E--> 370  cnanattggn nggccgcctc caaactttcn tcntnaaagg gncccaattc cccccnatt     720
E--> 371  aantggantt cctntttacc ttt                                           743
E--> 657  <210> SEQ ID NO: 32
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/12/2002
PATENT APPLICATION: US/10/004,115   TIME: 16:10:56

Input Set : A:\72249.txt
Output Set: N:\CRF4\08122002\J004115.raw

Skipped Sequences(NEW RULES):
Sequence(s)__missing. If intentional, please use the following format for
each skipped sequence.
<210> sequence id number
<400> sequence id number
000

Seq#:7,31

VARIABLE LOCATION SUMMARY   DATE: 08/12/2002
PATENT APPLICATION: US/10/004,115   TIME: 16:10:56

            Input Set : A:\72249.txt
            Output Set: N:\CRF4\08122002\J004115.raw

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:6; Xaa Pos. 6,7
Seq#:9; N Pos. 3,6,9
Seq#:10; N Pos. 3,6,9
Seq#:11; N Pos. 3,6,9
Seq#:12; N Pos. 3,6,9
Seq#:13; N Pos. 3,6,9
Seq#:14; N Pos. 3,6,9
Seq#:15; N Pos. 14,63,116,148,185,235,346,460,463,485,489,491,520,524,593
Seq#:15; N Pos. 602,682
Seq#:18; N Pos. 14
Seq#:19; N Pos. 434,440,443,448,458,467,475,506,510,517,522,533,535,583,584
Seq#:19; N Pos. 607,616,634,639,648,651,652,659,662,664,670,671,690,693,695
Seq#:19; N Pos. 702,717,723,728,734

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/004,115

DATE: 08/12/2002
TIME: 16:10:56

Input Set : **A:\72249.txt**
Output Set: **N:\CRF4\08122002\J004115.raw**

```
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:39 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:201 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:209 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:212 M:214 E: (33) Seq.# missing, SEQ ID NO:7
L:234 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:234 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:246 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:246 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:258 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:258 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:294 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:294 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:302 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:346 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:366 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
M:340 Repeated in SeqNo=19
L:657 M:214 E: (33) Seq.# missing, SEQ ID NO:31
```